Ex12	I NTp16.2 n <sup>2</sup> 1
CGGAGAGG	
CGAGAACA	Fx1 24
	ACGGCCGCGCCCGGGGTCGGGTAGAGGAGGTGCGGGCGCTGCTG Ex13
	NTp16.3
	GAGGCGGTGGCGCCAACGCACCGAATAGTTACGGTCGGAG
	I(2) I(1) Ex14
	GCCGATCCAGGTCATGGATGATGGGCAGCGCCCCGAGTGGCGGAG
	Ex2 Exon 2
	CTGCTGCTCCACGGCGCGAGCCCAACTGCGCCGACCCCGCCA
•	p16INT
	CTCTCACCCGACCCGTGCACGACGCTGCCCGGGAGGGCTTCTGGAC
====	NTp16.5
	ACGCTGGTGCTGCACCGGGCCGGGCCGGCTGGACGTGCGC
Ô	Ex3
	GATGCCTGGGGCCGTCTGCCCGTGGACCTGGCTGAGGAGCTGGGC
	CATCGCGATGTCGCACGGTACCTGCGCGCGGCTGCGGGGGGCACC
	Ex15 I(3)
	AGAGGCAGTAACCATGCCCGCATAGATGCCGCGGAAGGTCCCTC
	I(2) Ex8 Ex4
	AGACATCCCGATTGAAAGAACCAGAGAGGCTCTGAGAAACCTC
	Ex5
	GGGAAACTTAGATCATCAGTCACCGAAGGTCCTACAGGGCCACA
	ACTGCCCCGCCACAACCCACCCCGCTTTCGTAGTTTTCATTTAGA
	AAATAGAGCTTTTAAAAATGTCCTGCCTTTTAACGTAGATATAA
	GCCTTCCCCCACTACCGTAAATGTCCATTTATATCATTTTTATAT

Fig. 1A



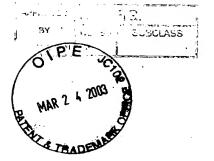
Fig. 1B



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p16EX1	< GGNGGNAAGNTGTGGGGAAAGTTTGGGGATGGAANACCAANCCCTCCTTTCNTTACCAA	60
	+	
p16EX1	< ACNCTGGCTCTGNCGAGGCTNCNTCCGANTGGTNCCCCCGGGGGAGACCCAACCTGGGNC	120
p16EX1 p16EX13	<pre>&lt; GACTTCAGGGNTGCNACATTCACTAAGTGCTNGGAGNTAATANCACCTCCTCCGAGCANx &lt; TCNCTTATTGNTAGGANATAATAACACCCCCGACCGALAACT</pre>	180 41
	+	
p16EX1 p16EX13	<pre>&lt; TCGCTCACAGCGTCCCCTTACCTNGANAGATACCNCGxGxTCCCTCCAGAGGATTTGAGG &lt; TcaCTTACAACGTCCCNNTtCCTGgaAAGATACacaGCGTTCCCTCCAGAGGATTTGTGG</pre>	240 101
	+	
p16EX1 p16EX13	< GACAGGNTCGGAGGGGCTCTTCCCCCANCACCGGAGGAAGAAAGAGGAGGGCTGACTG< GACAGGGTNGGAGNGGTCTCTTCCNCCACCACCGGAGGAAGAAAGAGGAGGGGCTGNCTG	300 161
	+ Ex1A (12)	
p16EX1 p16EX13	< GTCACCAGAGGGTGGGACCGCGTGCGCTCGGCGNCTNCGGAGAGGGGGAGAACAGA< TTCACCAGAGGGTGGGACCGCTACGCTCGNCGNCTNCGGAGAGGGGGAGAGCAGT	360 221
	t	
p16EX1 p16EX13	< CAACGGGCGGGGAGCAGCATGGATCCGGCGGGGGAGCAGCATGGANCCTTCGACT< CANCGGNCGNCGGGGAGCAACATGGAACCGNCGGCGGGGAGCAGCATGGANCCTTCGGCT	420 281
P16NT2 p16EX1	GACNNNCTCCGGCCGGNGTCGGGTAGAGGAGGTGCGGGCGCTGCTGGAG GACTGACTGCCTCGC	49 435
p16EX13	< GACTGGCTGNCCACGNCCCGGGGTCGGGTAGAGGAGGTGCGGNCGCTNCTGGAG	341
	t	
P16NT3 P16NT2	> Ex13 GTCTNANCCCGGGTA < GCGGGGGCGCTGCCCAACGCACCGAATAGTTACGGTCGGAGGCCGATCCAGGTxxGGGTA	15 109
p16EX13	< GCGGGGCTCTCTGCCCAACGCCTAAAAN	369
P16NT3 P16NT2	> GAGGGTCTGCAGCGGGAGCAGNGGATGGCGGGCGACTCTGGAGGACGAAGTTTGCAGGGG < GAGGGTCTGCAGCGGGAGCAGGGGATGGCGGGCGACTCTGGAGGACGAAGTTTGCAGGGG	75 169
P16NT3 P16NT2	> AATTGGAATCAGGTAGCGCTTCGANTCTCCGGAAAAAGGGGAGGCTTCCTGGGGAGTTNN < AATTGGAATCAGGTAGCGCTTCGATTCTCCNGAAAAAGGGGAGGCTTCCTGGGGAGTTTT	135 229

Fig. 2A



	$\cdots\cdots\cdots+\cdots\cdots+\cdots\cdots+\cdots\cdots+\cdots\cdots+\cdots\cdots+\cdots\cdots+\cdots\cdots+\cdots\cdots+\cdots\cdots+\cdots\cdots+\cdots\cdots+\cdots\cdots$	
	${\tt CAGAAGGGGTTTGTAATCACAGNCCTCCNCCTGGCGACGCCCTGGGGGGTTGGGAAGCCACAGAAGGGGTTTGTAATCACAGACCTCCTCCTGGCGACGTCCTGGGGGGCTTGGGAAGCCACAGAAGGGGGTTTGTAATCACAGACCTCCTCCTGGCGACGTCCTGGGGGGCTTGGGAAGCCACAGAAGGGGGTTTGGGAAGCCACAGAAGGGGGTTTGGGAAGCCACAGAAGGGGGTTTGGGAAGCCACAGAAGGGGGTTTGGGAAGCCACAGAAGGGGGTTTGGGAAGCCACAGAAGGGGGTTTGGGAAGCCAAGAAGGGGGTTTGGGAAGCCAAGAAGGGGGTTTGGGAAGCCAAGAAGGGGGTTTGGGAAGCCAAGAAGGGGGGTTTGGGAAGCCAAGAAGGGGGGTTTGGGAAGCCAAGAAGGGGGGTTTGGGAAGCCAAGAAGGGGGGTTTGGGAAGCCAAGAAGGGGGGTTTGGGAAGCCAAGAAGGGGGGTTTGGGAAGCCAAGAAGGGGGGTTTGGGAAGCCAAGAAGGGGGGTTGGGAAGCCAAGAAGGGGGGTTGGGAAGCCAAGAAGGGGGGTTGGGAAGCCAAGAAGGGGGGGTTGGGAAGCCAAGAAGGGGGGGG$	
	+	
		255 349
	+	
:	$\label{eq:ggggaacatatttgtattag} $$ $$ $ $ GGGGGAACATATTTGTATTAGXATNNAAGTATGCTCTTTATCAGATACAAAATTCACGAAGGGGGAACATATTTGTATTAGCNTCCAAGTNTNCTCTNTATCANATACAAANTXC $$ $$ $$ $ $ $ $ $ $ $ $ $ $ $ $ $ $ $	315 404
•	$\tt CGTGTGGNATAAAAAGGGAGTCTTAAAGAAATNTAAGATGTGCTGGGACTACTTAGCCTC$	375
,	CAANACACAGATNCCTGGATGGAGCT	401

Fig. 2B



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P16INT	> AAA	ANNAAAAAAATCTCCCAGGCCTAACATAATTNTCAGGAAAGAAATTTCAGTAGTTG	60
	• • •	+	
P16INT	> NAT	$\tt CTCAGGGGAAATACAGGAAGTTAGCCTGGAGTAAAAGTCAGTC$	120
	• • •		
P16INT	> TGC	TANATTGCCCGTGCCTCACAGTGCTCTCTGCCTGTGACGACAGCTCCNCAGAAGTTC	180
P16INT	> GGA	GGATATAATGGAATTCATTGTGTACTGAAGAATGGATAGAGAACTCAAGAAGGAAAT	240
	• • • •	+	
P16INT		AAACTGGAAGCAAATGTAGGGGTAATTAGACACCTGGGGGCTTGTGTGGGGGGTCTGCT	300
p16EX15	<	AANAAAAAAAATNGAtAANATagAGGAaT	31
		Ex2A	
P16INT p16EX15	> TGG( < gAA(	CGGTGAGGGGGCTCTACACAAGCTTCCTTTCCGTCATGCCGNCCCCCACCCTGGCTCCANATTAAAAAACGAGAATGTTcTAGAG	360 91
_		+	
P16INT		I Ex14 CCATTCTGTTCTCTGGCAGGTCATGATGATGGCAGCGCCCGAGTGGCGGAGCTG	420
p16EX15	< NTA	ATCATAATTATAAaggTcAAgACTCATTGATATAAAGGAaATtgAAGGGAAATctTa	151
	•••	+	
P16INT		CTGCTCCACGGCGCGGAGCCCAACTGCTCCGACGCCG	460
p16EX2 p16EX14	> >	CCTGCNACGACCCCGCCACTCTCACCCGACCCGTG	
p16EX15		NCTCTCACGGTGGGGAGGCCAACTGCGCCGAACCCGCCACTCTCACCCGACCCGCGAGCACACAANNGNATNAAAAAANAATTcCCACGACACGCCACTCTCAACCGATCCGTG	56 211
••	• • • •		•
p16EX2	> CACC	GACGCTGTCCGGGAGGGTTTCCTGGACACGCTGGTGGTGCTGCACCGGGCCGGGGNG	95
p16EX14 p16EX15	> CACC	BACGGTGCCCGGGAGGGGTTCCTGGACACGCTGGTGGTGCTGCACCGGGCCGGGGCGGGC	116
Promis			2/1
	• • • •	+	
p16EX2	> CGGT	TTGGACGTGCGCGATGCCTGGGGCCGCCTNCCCGTGGxACCTGGTTGAGGAGCTGGG	155
p16EX14 p16EX15	< CGTC	CTGGACGTTCGNGATGCCTGGGGGCNTCTNTCCGTNGxACCTGGCTGAAGAGCTGGN CTGGACGTGCGCGATGCCTGGGNCCGNCTACCCGTGGTACCTGACTGAGGACCTGGG	176 331
		+	
p16EX2	> NCAT	CGCGATGTCGCACGGTACCTGCGCGCGGTTGCGGGGGGCACCAGAGGxNAGTNACC	215
p16EX14	> NCAT	CGNGATGTCGCACGGCCNCTGTGTGNGGNTGCGGGGGGCACCATAGGTCAGTNTCC	236
p16EX15	< CCA'I	CCCGATTTCGCNGGGTANCTGNGNGNGGCTGNGGGGGCCAANAGAGGxCANTACCC	391

Fig. 2C

SUBCLASS

p16EX4

p16EX9

< AA

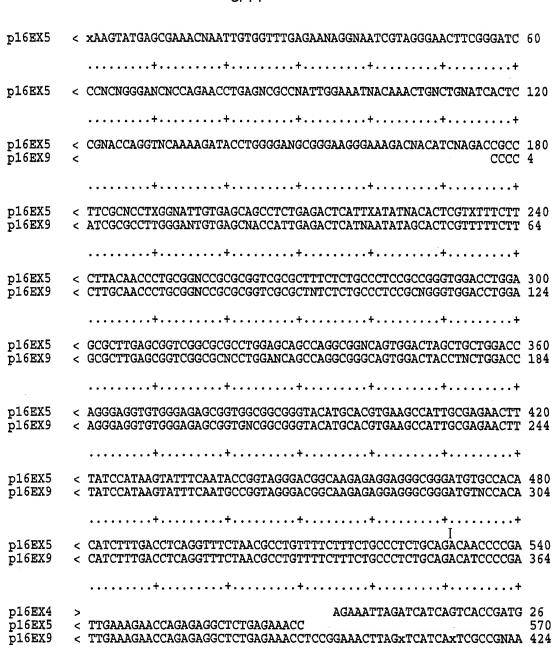


Fig. 3A

......+.

> GTCCTACAGGGNCACAACTGNCCCCGCCACACCCACCCCGNTTTCGTAGTTTTCATTTA 86

426

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p16EX4	>	GAAAATAGAGCTTTTAAAAAATGTCCTGCCTTTTAACGTAGATATATGCCTTCCCCCACTA	146
		$\cdots\cdots\cdots+$	
p16EX4	>	${\tt CCGNAAATGTCCATTTATATCATNTTTTATATATTCTTATAAAAAATGTAAAAAAAAAA$	206
		+	
p16EX4	>	${\tt CACCGCTTCTGCCTTTTCACTGTTTGGAGTTTTCTGGAGTGAGCACTCACGCCCTAAGC}$	266
		+	
p16EX6 p16EX6a p16EX4	> >	CANCNATNTNCGGCATTTCTNGNGAGCCTCGTAGTCTCCGGATGNTGTCGACCTCGAG CANCNATNTNCGGCATTTCTNGNGAGCCTCGTAGTCTCCGGATGNTGTCGACCTCGAG GCACATTCATGTGGGCATTTCTTGCGAGCCTCGCAGNCTCCGGAAGCTGTCGAC	58
p16EX6 p16EX6a p16EX4	>	GGGGGGNCCNGTACCCAATTCGNCCTATNGTGAGTCGTNTTACAATTCACTGGCCGCCGT GGGGGGNCCNGTACCCAATTCGNCCTATNGTGAGTCGTNTTACAATTCACTGGCCGCCGT GGGGGGNCCGGTACCCAATTCGCCCTATAGTGAGTCGTATTACAATTCACTGGNCGNCGN	118 118 386
		+	
p16EX6 p16EX6a p16EX4	>	$\label{totalcolor} \textbf{TTT} \textbf{A} \textbf{C} \textbf{C} \textbf{C} \textbf{C} \textbf{T} \textbf{G} \textbf{A} \textbf{A} \textbf{A} \textbf{C} \textbf{C} \textbf{C} \textbf{T} \textbf{G} \textbf{C} \textbf{C} \textbf{T} \textbf{G} \textbf{A} \textbf{A} \textbf{C} \textbf{C} \textbf{C} \textbf{T} \textbf{G} \textbf{C} \textbf{A} \textbf{C} \textbf{T} \textbf{T} \textbf{A} \textbf{A} \textbf{T} \textbf{C} \textbf{G} \textbf{C} \textbf{C} \textbf{T} \textbf{G} \textbf{A} \textbf{A} \textbf{A} \textbf{C} \textbf{C} \textbf{C} \textbf{G} \textbf{G} \textbf{G} \textbf{T} \textbf{T} \textbf{A} \textbf{A} \textbf{T} \textbf{C} \textbf{G} \textbf{C} \textbf{C} \textbf{T} \textbf{T} \textbf{G} \textbf{A} \textbf{G} \textbf{C} \textbf{C} \textbf{C} \textbf{G} \textbf{G} \textbf{G} \textbf{G} \textbf{G} \textbf{G} \textbf{G} G$	
		+	
p16EX6 p16EX6a p16EX4	>	NACATCCCCCTTTxCGCCAGCTGGTGTAATAGCGANGAGGCCCGCACCGATCGCCCTTCC NACATCCCCCTTTxCGCCAGCTGGTGTAATAGCGANGAGGCCCGCACCGATCGCCCTTCC GACATCCCCCTTTTCGCCAGNTGGGGTTAATAGNGAAGAGGGCCNCACCNNTCGCCC	238 238 502
		+	
p16EX6 p16EX6a		${\tt CAACAGTTGNGCAGCCTGAATGGCGAATGGAAATTGTAAGCGTTAATATTTTGTTAAAAT}\\ {\tt CAACAGTTGNGCAGCCTGAATGGCGAATGGAAATTGTAAGCGTTAATATTTTGTTAAAAT}\\$	298 298
		+++	
p16EX6 p16EX6a		${\tt TCGCGTTANATCNTCGGTTAANTCAGCTCATNTTTTATCCAATAGGCCGANATCGGCANATCGCGTTANATCNTCGGTTAANTCAGCTCATNTTTTATCCAATAGGCCGANATCGGCANAT$	
p16EX6 p16EX6a		ATCCCCAATAAATCAANAGAATAGACCGAGATAGGGTTGAGTGTCGTTCCAGTTNGGGAA ATCCCCAATAAATCAANAGAATAGACCGAGATAGGGTTGAGTGTCGTTCCAGTTNGGGAA	
ř			
p16EX6 p16EX6a	. >	CANGAGTCCACTATTAAAGANCGTAGNCTCNAACGTCANAGGGCGAAAAACCNTNTTTCA CANGAGTCCACTATTAAAGANCGTAGNCTCNAACGTCANAGGGCGAAAAACCNTNTTTCA	478 478



## 8/11

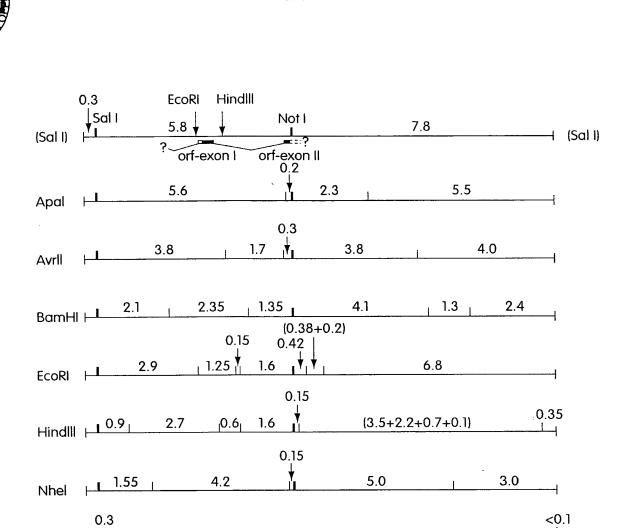
p16EX6	> GNGGATTGGNCCACTACGCNTANCC > GNGGATTGGNCCACTACGCNTANCCATCACCCTATTC		503 515					
p16EX6a	>	GNGGATTGGNCCACTACG	CNTANCCATC	ACCCTATTC	•			515
		-L	.1.		_	.1.		

Fig. 3C



	0/ /	•	
CELL	EXON 1 EXON 2	CEIL	EXON 1 EXON 2
NORMAL #2	NORM	HTB173	NORM
NORMAL #1	NORM	HTB172	NORM
A431	ALTERED ABSENT	Tera2	NORM
SaOs2	ALTERED ALTERED	GM130	NORM
HTB 125	ABSENT	ZRB75	NORM
MCF-7	ABSENT ABSENT	HTB100	NORM
CCL119	ABSENT	HeLa	NORM
018	ABSENT	CCL120	NORM
H9	ABSENT ABSENT	WI38	NORM

Fig. 4



Pstl | 1.1+0.8 | 3.6 | 5.6 | (1.5+0.7) |

Sacl | 1.25 | 4.55 | 0.5 | (6.0+0.56+0.34) | 0.9 |

Xbal | 4.7 | 0.2 | 2.8 |

Fig. 5

Ile Gln Val Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Met Met Met Gly Asn Val His Val Ala Ala Leu Leu Leu Asn Tyr Gly Ala Asp Ser Asn Cys Glu Asp Pro \* p16: p15: p13:

Arg Arg Arg Ala Ala Val Leu His Arg Ala Gly Val Leu His Arg Ala Gly Val Leu His Gly Ser Gly Leu Val Leu Val Leu Val Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Arg Arg Arg Thr Thr Ser Phe Thr Leu Thr Leu Thr Thr 1

Arg Arg Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu Glu Arg Gly His Arg Asp Val Ala Gly Tyr Leu Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Leu Asp Leu Ala Glu Arg Gly His Gln Asp Ile Val Arg Tyr Leu

Thr Ala Ala Ala Gly Gly : Thr Ala Thr Gly Asp Ser Ala \* Gly Cys & GLy

Cys Ser

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